```
********************
***   TX REPORT   ***
********************
```

#9

TRANSMISSION OK

TX/RX NO   2517
CONNECTION TEL   912126618002
SUBADDRESS
CONNECTION ID   BIERMANMUSERLIAN
ST. TIME   04/26 07:03
USAGE T   02'52
PGS. SENT   6
RESULT   OK

UNITED STATES PATENT AND ★★★★ TRADEMARK OFFICE

PCT OPERATIONS

FACSIMILE TRANSMISSION COVER SHEET

DATE: 26 Apr 02

TO: Charles A. Muserlian

TELEPHONE: 212-661 8000
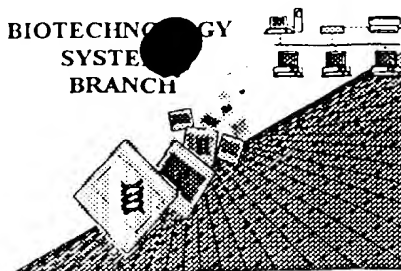FAX NO.: 212-661-8002

FROM: Charitta Burt

TELEPHONE: 703-305-3734
FAX NO.: 703-308-4785 OR 703-305-3230

UNITED STATES PATENT AND TRADEMARK OFFICE

PCT OPERATIONS

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FAX NO.: 703-308-4785 OR 703-305-3230

MESSAGE: _____

_____

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NUMBER OF PAGES 6 (INCLUDING THIS PAGE)

RAW SEQUENCE LISTING
ERROR REPORT

Bur

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/674,109_

Source: _Pct 09_

Date Processed by STIC: _5-29-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

PCT*O*

RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: US/09/674,109   TIME: 15:37:28

Input Set : A:\SeqListing.APP.txt
Output Set: C:\CRF3\05292001\I674109.raw

    3 <110> APPLICANT: HOECHST MARION ROUSSEL
    5 <120> TITLE OF INVENTION: METHOD FOR SCREENING ANTIMYCOTIC SUBSTANCES USING
    6   ESSENTIAL GENES FROM S.CEREVISIAE
    8 <130> FILE REFERENCE: 16363PC RUU 7

Does Not Comply
Corrected Diskette Needed

-> 10 <140> CURRENT APPLICATION NUMBER: US/09/674,109
-> 11 <141> CURRENT FILING DATE: 2000-11-22
   13 <150> PRIOR APPLICATION NUMBER: 98402254.1
   14 <151> PRIOR FILING DATE: 1998-09-11
   16 <150> PRIOR APPLICATION NUMBER: 98401007.4
   17 <151> PRIOR FILING DATE: 1998-04-24
-> 19 <160> NUMBER OF SEQ ID NOS: 180
   21 <170> SOFTWARE: PatentIn Ver. 2.1

:RORED SEQUENCES

  1337 <210> SEQ ID NO: 106   *Seq #106, number of bases differ:*
  1338 <211> LENGTH: (62)   *- 62 listed*
  1339 <212> TYPE: DNA   *- 59 shown*
  1340 <213> ORGANISM: Artificial Sequence
  1342 <220> FEATURE:
  1343 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
  1344   YML049c-S1
  1346 <400> SEQUENCE: 106
-> 1347 aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc (59)
  1474 <210> SEQ ID NO: 117   *Seq #117, number of bases differ*
  1475 <211> LENGTH: (59)   *- 59 listed*
  1476 <212> TYPE: DNA   *- 62 shown*
  1477 <213> ORGANISM: Artificial Sequence
  1479 <220> FEATURE:
  1480 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
  1481   YMR211w-S2
  1483 <400> SEQUENCE: 117
  1484 atttcaatca tcttactccg tgaatcaggt tcggaatgat gcataggcca ctagtggatc 60
-> 1485 tg   (62)
  2265 <210> SEQ ID NO: 180
  2266 <211> LENGTH: 62
  2267 <212> TYPE: DNA
  2268 <213> ORGANISM: Artificial Sequence
  2270 <220> FEATURE:
  2271 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
  2272   YPR137w-S2
  2274 <400> SEQUENCE: 180
  2275 aaaagcctgt ttggtcaatg acagctgaat atataccatt gcataggcca ctagtggatc 60
  2276 tg   62
-> 2279 imer
-> 2280   ymr290c-s1

Input Set : A:\SeqListing.APP.txt
Output Set: C:\CRF3\05292001\I674109.raw

```
--> 2282 <210> SEQ ID NO:
--> 2282 <211> LENGTH:
--> 2282 <212> TYPE:
--> 2282 <213> ORGANISM:
--> 2282 <400> SEQUENCE: 105
     2283 tgagttttac gtcttttggt atttggcgtt tttccactgg cagctgaagc ttcgtacgc  59
     2285 <210> SEQ ID NO: 106
     2286 <211> LENGTH: 62
     2287 <212> TYPE: DNA
     2288 <213> ORGANISM: Artificial Sequence
     2290 <220> FEATURE:
     2291 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
     2292        YML049c-S1
     2294 <400> SEQUENCE: 106
--> 2295 aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc  59
     2422 <210> SEQ ID NO: 117
     2423 <211> LENGTH: 59
     2424 <212> TYPE: DNA
     2425 <213> ORGANISM: Artificial Sequence
     2427 <220> FEATURE:
     2428 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
     2429        YMR211w-S2
     2431 <400> SEQUENCE: 117
     2432 atttcaatca tcttactccg tgaatcaggt tcggaatgat gcataggcca ctagtggatc  60
--> 2433 tg                                                                62
```

Disregard, these are errors due to the duplication of sequences 105 to 153 as shown on p. 3.

<210> 180 → *Seq. 180 - listed as last on the file.*
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
      YPR137w-S2

| <400> (180)
aaaagcctgt ttggtcaatg acagctgaat atataccatt gcataggcca ctagtggatc 60
tg

After sequence 180, the listing starts over at sequence # 105 and goes to sequence # 153. All of this duplication must be deleted from the file.

delete ~~imer~~

~~YMR290c-S1~~

<400> (105)
tgagttttac gtcttttggt atttggcgtt tttccactgg cagctgaagc ttcgtacgc   59

<210> 106
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
      YML049c-S1

<400> 106
aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc   59

<210> 107
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
      YMR290c-S2

<400> 107

VERIFICATION SUMMARY   DATE: 05/29/2001
PATENT APPLICATION: **US/09/674,109**   TIME: 15:37:30

Input Set : **A:\SeqListing.APP.txt**
Output Set: **C:\CRF3\05292001\I674109.raw**

```
:10 M:270 C: Current Application Number differs, Replaced Application Number
:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
:1347 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:59 SEQ:106
:1485 M:252 E: No. of Seq. differs, <211>LENGTH:Input:59 Found:62 SEQ:117
:2279 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
:2280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:180
:2280 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:68 SEQ:180
:2280 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
:2280 M:112 C: (48) String data converted to lower case,
:2280 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:68 SEQ:180
:2282 M:282 W: Numeric Field Identifier Missing, <210> is required.
:2282 M:282 W: Numeric Field Identifier Missing, <211> is required.
:2282 M:282 W: Numeric Field Identifier Missing, <212> is required.
:2282 M:282 W: Numeric Field Identifier Missing, <213> is required.
 2282 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:180 differs:105
 2295 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:59 SEQ:106
:2433 M:252 E: No. of Seq. differs, <211>LENGTH:Input:59 Found:62 SEQ:117
:19 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (180) Counted (228)
```